SEQUENCE LISTING

<110> MUSC Foundation For Research Development

<120> Complement Receptor 2 Targeted
  Complement Modulators

<130> 19113.0095P1

<150> 60/426,676
<151> 2002-11-15

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1041.
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
     synthetic construct

<400> 1
gactgtggcc ttcccccaga tgtacctaat gcccagccag ctttggaagg ccgtacaagt 60
tttcccgagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 120
gagaaggact cagtgatctg ccttaagggc agtcaatggt cagatattga agagttctgc 180
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 240
actcagaatt attttccagt cggtactgtt gtggaatatg agtgccgtcc aggttacaga 300
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 360
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 420
gatgtaccag gtggcatatt atttggtgca accatctcct tctcatgtaa cacagggtac 480
aaattatttg gctcgacttc tagttttgt cttatttcag gcagctctgt ccagtggagt 540
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 600
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcatgtaat 660
aaaggattca ccatgattgg agagcactct atttattgta ctgtgaataa tgatgaagga 720
gagtggagtg gcccaccacc tgaatgcaga ggaaaatctc taacttccaa ggtcccacca 780
acagttcaga aacctaccac agtaaatgtt ccaactacag aagtctcacc aacttctcag 840
aaaaccacca caaaaaccac cacaccaaat gctcaagcaa cacggagtac acctgtttcc 900
aggacaacca agcattttca tgaaacaacc ccaaataaag gaagtggaac cacttcaggt 960
actacccgtc ttctatctgg gcacacgtgt ttcacgttga caggtttgct tgggacgcta 1020
gtaaccatgg gcttgctgac t   1041

<210> 2
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
     synthetic construct

<400> 2
Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu Gly
 1   5   10   15
Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val
             20   25   30

1

```
Trp Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu
        35                  40                  45
Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys
    50                  55                  60
Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys
65                  70                  75                  80
Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser
                85                  90                  95
Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr
            100                 105                 110
Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys
        115                 120                 125
Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys
    130                 135                 140
Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Lys
145                 150                 155                 160
Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro
                165                 170                 175
Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly
                180                 185                 190
Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser
        195                 200                 205
Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys
    210                 215                 220
Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp
225                 230                 235                 240
His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe
            245                 250                 255
Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu
            260                 265                 270
Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu Thr
        275                 280                 285
Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val Pro
    290                 295                 300
Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr Thr
305                 310                 315                 320
Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr Thr
            325                 330                 335
Lys His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr Ser
            340                 345                 350
Gly Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly
        355                 360                 365
Leu Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
370                 375                 380
```

<210> 3
<211> 306
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
    synthetic construct

<400> 3
cagtgctaca actgtcctaa cccaactgct gactgcaaaa cagccgtcaa ttgttcatct 60
gattttgatg cgtgtctcat taccaaagct gggttacaag tgtataacaa gtgttggaag 120
tttgagcatt gcaatttcaa cgacgtcaca acccgcttga gggaaaatga gctaacgtac 180
tactgctgca agaaggacct gtgtaacttt aacgaacagc ttgaaaatgg tgggacatcc 240
ttatcagaga aaacagttct tctgctggtg actccatttc tggcagcagc ctggagcctt 300

2

catcc   306

```
<210> 4
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 4
Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu
 1               5                  10                  15
Ala Val Phe Cys His Ser Gly His Gln Cys Tyr Asn Cys Pro Asn Pro
            20                  25                  30
Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe Asp Ala
        35                  40                  45
Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys
    50                  55                  60
Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg Glu Asn
65                  70                  75                  80
Glu Leu Thr Tyr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu
            85                  90                  95
Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val Leu Leu
            100                 105                 110
Leu Val Thr Pro Phe Leu Ala Ala Ala Trp Ser Leu His Pro
        115                 120                 125
```

```
<210> 5
<211> 1485
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 5
atttcttgtg gctctcctcc gcctatccta aatggccgga ttagttatta ttctacccc   60
attgctgttg gtaccgtgat aaggtacagt tgttcaggta ccttccgcct cattggagaa  120
aaaagtctat tatgcataac taaagacaaa gtggatggac cctgggataa acctgctcct  180
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac  240
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc  300
aacttctcca tgaacggaaa caagtctgtt tggtgtcaag caaataatat gtggggccg   360
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc  420
cacaatggac atcacacaag tgagaatgtt ggctccattg ctccaggatt gtctgtgact  480
tacagctgtg aatctggtta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg  540
ggaaaatgga gtgctgtccc ccccacatgt gaagaggcac gctgtaaatc tctaggacga  600
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaacttt  660
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga  720
cagggagttg cttggaccaa aatgccagta tgtggaggtg ggtcgggtgg cggcggatcc  780
gactgtggcc ttcccccaga tgtacctaat gcccagccag ctttggaagg ccgtacaagt  840
tttcccgagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc  900
gagaaggact cagtgatctg ccttaagggc agtcaatggt cagatattga agagttctgc  960
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 1020
actcagaatt attttccagt cggtactgtt gtggaatatg agtgccgtcc aggttacaga 1080
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg tccacagca  1140
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 1200
gatgtaccag gtggcatatt atttggtgca accatctcct tctcatgtaa cacagggtac 1260
```

3

```
aaattatttg gctcgacttc tagttttttgt cttatttcag gcagctctgt ccagtggagt 1320
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 1380
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcatgtaat 1440
aaaggattca ccatgattgg agagcactct atttattgta ctgtg        1485
```

<210> 6
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 6
```
Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr
 1               5                  10                  15
Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser
            20                  25                  30
Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys
        35                  40                  45
Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr
    50                  55                  60
Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr
65                  70                  75                  80
Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe
                85                  90                  95
Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys
            100                 105                 110
Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser
        115                 120                 125
Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His
    130                 135                 140
His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr
145                 150                 155                 160
Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn
                165                 170                 175
Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu
            180                 185                 190
Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu
        195                 200                 205
Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu
    210                 215                 220
Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly
225                 230                 235                 240
Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Gly Gly Gly Ser Gly
                245                 250                 255
Gly Gly Gly Ser Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln
            260                 265                 270
Pro Ala Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr
        275                 280                 285
Tyr Lys Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser
    290                 295                 300
Val Ile Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys
305                 310                 315                 320
Asn Arg Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys
                325                 330                 335
Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu
            340                 345                 350
Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys
        355                 360                 365
```

```
Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys
    370                 375                 380
Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile
385                 390                 395                 400
Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys
                405                 410                 415
Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile
                420                 425                 430
Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu
        435                 440                 445
Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly
    450                 455                 460
Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn
465                 470                 475                 480
Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val
                485                 490                 495
```

```
<210> 7
<211> 1002
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 7
atttcttgtg gctctcctcc gcctatccta aatggccgga ttagttatta ttctaccccc  60
attgctgttg gtaccgtgat aaggtacagt tgttcaggta ccttccgcct cattggagaa 120
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac 240
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300
aacttctcca tgaacggaaa caagtctgtt tggtgtcaag caataatat gtgggggccg 360
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
cacaatggac atcacacaag tgagaatgtt ggctccattg ctccaggatt gtctgtgact 480
tacagctgtg aatctggtta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 540
ggaaaatgga gtgctgtccc ccccacatgt gaagaggcac gctgaaatc tctaggacga 600
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaacttt 660
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 720
cagggagttg cttggaccaa aatgccagta tgttcaggag gaggaggttc cctgcagtgc 780
tacaactgtc ctaacccaac tgctgactgc aaaacagccg tcaattgttc atctgatttt 840
gatgcgtgtc tcattaccaa agctgggtta caagtgtata caagtgttg gaagtttgag 900
cattgcaatt tcaacgacgt cacaacccgc ttgagggaaa atgagctaac gtactactgc 960
tgcaagaagg acctgtgtaa ctttaacgaa cagcttgaaa t                     1002
```

```
<210> 8
<211> 334
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 8
Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr
1               5                   10                  15
Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser
            20                  25                  30
```

```
Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys
        35                      40                      45
Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr
        50                      55                      60
Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr
65                      70                      75                      80
Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe
                85                      90                      95
Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys
            100                     105                     110
Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser
            115                     120                     125
Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His
        130                     135                     140
His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr
145                     150                     155                     160
Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn
                165                     170                     175
Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu
                180                     185                     190
Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu
            195                     200                     205
Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu
        210                     215                     220
Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly
225                     230                     235                     240
Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Ser Gly Gly Gly Gly
                245                     250                     255
Ser Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr
                260                     265                     270
Ala Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala
            275                     280                     285
Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe
        290                     295                     300
Asn Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys
305                     310                     315                     320
Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn
                325                     330
```

<210> 9
<211> 1554
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 9
```
gactgtggcc ttcccccaga tgtacctaat gcccagccag ctttggaagg ccgtacaagt 60
tttcccgagg atactgtaat aacgtacaaa tgtgaagaaa gctttgtgaa aattcctggc 120
gagaaggact cagtgatctg ccttaagggc agtcaatggt cagatattga gagttctgc 180
aatcgtagct gcgaggtgcc aacaaggcta aattctgcat ccctcaaaca gccttatatc 240
actcagaatt attttccagt cggtactgtt gtggaatatg agtgccgtcc aggttacaga 300
agagaacctt ctctatcacc aaaactaact tgccttcaga atttaaaatg gtccacagca 360
gtcgaatttt gtaaaaagaa atcatgccct aatccgggag aaatacgaaa tggtcagatt 420
gatgtaccag gtggcatatt atttggtgca accatctcct ctcatgtaa cacagggtac 480
aaattatttg gctcgacttc tagttttgt cttatttcag gcagctctgt ccagtggagt 540
gacccgttgc cagagtgcag agaaatttat tgtccagcac caccacaaat tgacaatgga 600
ataattcaag gggaacgtga ccattatgga tatagacagt ctgtaacgta tgcatgtaat 660
```

```
aaaggattca ccatgattgg agagcactct atttattgta ctgtgaataa tgatgaagga 720
gagtggagtg gcccaccacc tgaatgcaga tcctctggtg gcggtggctc gggcggaggt 780
gggtcgggtg gcggcggatc catttcttgt ggctctcctc cgcctatcct aaatggccgg 840
attagttatt attctacccc cattgctgtt ggtaccgtga taaggtacag ttgttcaggt 900
accttccgcc tcattggaga aaaaagtcta ttatgcataa ctaaagacaa agtggatgga 960
acctgggata aacctgctcc taaatgtgaa tatttcaata aatattcttc ttgccctgag 1020
cccatagtac caggaggata caaaattaga ggctctacac cctacagaca tggtgattct 1080
gtgacatttg cctgtaaaac caacttctcc atgaacggaa acaagtctgt ttggtgtcaa 1140
gcaaataata tgtgggggcc gacacgacta ccaacctgtg taagtgtttt ccctctcgag 1200
tgtccagcac ttcctatgat ccacaatgga catcacacaa gtgagaatgt tggctccatt 1260
gctccaggat tgtctgtgac ttacagctgt gaatctggtt acttgcttgt tggagaaaag 1320
atcattaact gtttgtcttc gggaaaatgg agtgctgtcc cccccacatg tgaagaggca 1380
cgctgtaaat ctctaggacg atttcccaat gggaaggtaa aggagcctcc aattctccgg 1440
gttggtgtaa ctgcaaactt tttctgtgat gaagggtatc gactgcaagg cccaccttct 1500
agtcggtgtg taattgctgg acagggagtt gcttggacca aaatgccagt atgt       1554
```

<210> 10
<211> 518
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
     synthetic construct

<400> 10
```
Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala Leu Glu
 1               5                  10                  15
Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys Cys Glu
            20                  25                  30
Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile Cys Leu
        35                  40                  45
Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg Ser Cys
    50                  55                  60
Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro Tyr Ile
65                  70                  75                  80
Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu Cys Arg
                85                  90                  95
Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr Cys Leu
            100                 105                 110
Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys Lys Ser
        115                 120                 125
Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val Pro Gly
    130                 135                 140
Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr Gly Tyr
145                 150                 155                 160
Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser
                165                 170                 175
Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr Cys Pro
            180                 185                 190
Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg Asp His
        195                 200                 205
Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly Phe Thr
    210                 215                 220
Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp Glu Gly
225                 230                 235                 240
Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Ser Ser Gly Gly Gly Gly
                245                 250                 255
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Ser Cys Gly Ser
            260                 265                 270
```

```
Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr Tyr Ser Thr Pro Ile
        275                 280                 285
Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser Gly Thr Phe Arg Leu
    290                 295                 300
Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys Asp Lys Val Asp Gly
305                 310                 315                 320
Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr Phe Asn Lys Tyr Ser
            325                 330                 335
Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr Lys Ile Arg Gly Ser
        340                 345                 350
Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe Ala Cys Lys Thr Asn
        355                 360                 365
Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys Gln Ala Asn Asn Met
    370                 375                 380
Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser Val Phe Pro Leu Glu
385                 390                 395                 400
Cys Pro Ala Leu Pro Met Ile His Asn Gly His His Thr Ser Glu Asn
            405                 410                 415
Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr Tyr Ser Cys Glu Ser
        420                 425                 430
Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn Cys Leu Ser Ser Gly
        435                 440                 445
Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu Ala Arg Cys Lys Ser
    450                 455                 460
Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu Pro Pro Ile Leu Arg
465                 470                 475                 480
Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu Gly Tyr Arg Leu Gln
            485                 490                 495
Gly Pro Pro Ser Ser Arg Cys Val Ile Ala Gly Gln Gly Val Ala Trp
        500                 505                 510
Thr Lys Met Pro Val Cys
        515
```

<210> 11
<211> 990
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 11
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ctgcagtgct acaactgtcc taacccaact gctgactgca aaacagccgt caattgttca  60
tctgattttg atgcgtgtct cattaccaaa gctgggttac aagtgtataa caagtgttgg 120
aagtttgagc attgcaattt caacgacgtc acaacccgct tgagggaaaa tgagctaacg 180
tactactgct gcaagaagga cctgtgtaac tttaacgaac agcttgaaaa ttcctctggt 240
ggcggtggct ccggcggagg tgggtccggt ggcggcggat ccatttcttg tggctctcct 300
ccgcctatcc taaatggccg gattagttat tattctaccc ccattgctgt tggtaccgtg 360
ataaggtaca gttgttcagg taccttccgc ctcattggag aaaaaagtct attatgcata 420
actaaagaca aagtggatgg aacctgggat aaacctgctc ctaaatgtga atatttcaat 480
aaatattctt cttgccctga gccatagta ccaggaggat acaaaattag aggctctaca 540
ccctacagac atggtgattc tgtgacattt gcctgtaaaa ccaacttctc catgaacgga 600
aacaagtctg tttggtgtca agcaaataat atgtgggggc cgacacgact accaacctgt 660
gtaagtgttt tccctctcga gtgtccagca cttcctatga tccacaatgg acatcacaca 720
agtgagaatg ttggctccat tgctccagga ttgtctgtga cttacagctg tgaatctggt 780
tacttgcttg ttggagaaaa gatcattaac tgtttgtctt cgggaaatg gagtgctgtc 840
cccccacat gtgaagaggc acgctgtaaa tctctaggac gatttcccaa tgggaaggta 900
aaggagcctc caattctccg ggttggtgta actgcaaact ttttctgtga tgaagggtat 960
cgactgcaag gcccaccttc tagtcggtgt                                  990
```

<210> 12
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 12
Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
 1   5   10   15
Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
            20   25   30
Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
        35   40   45
Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
    50   55   60
Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Ser Ser Gly
65   70   75   80
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Ser
            85   90   95
Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly Arg Ile Ser Tyr Tyr Ser
            100   105   110
Thr Pro Ile Ala Val Gly Thr Val Ile Arg Tyr Ser Cys Ser Gly Thr
        115   120   125
Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu Cys Ile Thr Lys Asp Lys
    130   135   140
Val Asp Gly Thr Trp Asp Lys Pro Ala Pro Lys Cys Glu Tyr Phe Asn
145   150   155   160
Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val Pro Gly Gly Tyr Lys Ile
            165   170   175
Arg Gly Ser Thr Pro Tyr Arg His Gly Asp Ser Val Thr Phe Ala Cys
            180   185   190
Lys Thr Asn Phe Ser Met Asn Gly Asn Lys Ser Val Trp Cys Gln Ala
        195   200   205
Asn Asn Met Trp Gly Pro Thr Arg Leu Pro Thr Cys Val Ser Val Phe
    210   215   220
Pro Leu Glu Cys Pro Ala Leu Pro Met Ile His Asn Gly His His Thr
225   230   235   240
Ser Glu Asn Val Gly Ser Ile Ala Pro Gly Leu Ser Val Thr Tyr Ser
            245   250   255
Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu Lys Ile Ile Asn Cys Leu
            260   265   270
Ser Ser Gly Lys Trp Ser Ala Val Pro Pro Thr Cys Glu Glu Ala Arg
        275   280   285
Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly Lys Val Lys Glu Pro Pro
        290   295   300
Ile Leu Arg Val Gly Val Thr Ala Asn Phe Phe Cys Asp Glu Gly Tyr
305   310   315   320
Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
            325   330

<210> 13
<211> 5994
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 13
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ttttctatca tctgcctaaa aaactcagtc tggactggtg ctaaggacag gtgcagacgt 180
aaatcatgtc gtaatcctcc agatcctgtg aatggcatgg tgcatgtgat caaaggcatc 240
cagttcggat cccaaattaa atattcttgt actaaaggat accgactcat tggttcctcg 300
tctgccacat gcatcatctc aggtgatact gtcatttggg ataatgaaac acctatttgt 360
gacagaattc cttgtgggct acccccacc atcaccaatg gagatttcat tagcaccaac 420
agagagaatt ttcactatgg atcagtggtg acctaccgct gcaatcctgg aagcggaggg 480
agaaaggtgt ttgagcttgt gggtgagccc tccatatact gcaccagcaa tgacgatcaa 540
gtgggcatct ggagcggccc cgcccctcag tgcattatac ctaacaaatg cacgcctcca 600
aatgtggaaa atggaatatt ggtatctgac aacagaagct tattttcctt aaatgaagtt 660
gtggagttta ggtgtcagcc tggctttgtc atgaaaggac cccgccgtgt gaagtgccag 720
gccctgaaca aatgggagcc ggagctacca agctgctcca gggtatgtca gccacctcca 780
gatgtcctgc atgctgagcg tacccaaagg gacaaggaca acttttcacc tgggcaggaa 840
gtgttctaca gctgtgagcc cggctacgac ctcagagggg ctgcgtctat gcgctgcaca 900
ccccagggag actggagccc tgcagccccc acatgtgaag tgaaatcctg tgatgacttc 960
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ttggctggaa tggaaagcct ttggaatagc agtgttccag tgtgtgaaca aatctttgt 1140
ccaagtcctc cagttattcc taatgggaga cacacaggaa aacctctgga agtctttccc 1200
tttggaaaag cagtaaatta cacatgcgac ccccacccag acagagggac gagcttcgac 1260
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agccctgccc ctcgctgtgg aattctgggt cactgtcaag ccccagatca ttttctgttt 1380
gccaagttga aaacccaaac caatgcatct gactttccca ttgggacatc tttaaagtac 1440
gaatgccgtc ctgagtacta cgggaggcca ttctctatca catgtctaga taacctggtc 1500
tggtcaagtc ccaaagatgt ctgtaaacgt aaatcatgta aaactcctcc agatccagtg 1560
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caggttggat ccagaatcaa ctattcttgt actacagggc accgactcat tggtcactca 3000
tctgctgaat gtatcctctc aggcaatact gcccattgga gcacgaagcc gccaatttgt 3060
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agaaaggtgt ttgagcttgt gggtgagccc tccatatact gcaccagcaa tgacgatcaa 3240
gtgggcatct ggagcggccc cgcccctcag tgcattatac ctaacaaatg cacgcctcca 3300
aatgtggaaa atggaatatt ggtatctgac aacagaagct tattttcctt aaatgaagtt 3360
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gaaatcctgc atggtgagca taccccaagc catcaggaca acttttcacc tgggcaggaa  3540
gtgttctaca gctgtgagcc tggctatgac ctcagagggg ctgcgtctct gcactgcaca  3600
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ttgaattatg aatgccgtcc tgggtatttt gggaaaatgt tctctatctc ctgcctagaa  4200
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acggtggtaa cttaccagtg ccacactgga ccagatggag aacagctgtt tgagcttgtg  4560
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aataatgcac atgaaaaccc taaagaagtg gctatccatt acattctca aggaggcagc  5940
agcgttcatc cccgaactct gcaaacaaat gaagaaaata gcagggtcct tcct         5994
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<210> 14
<211> 2048
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
     synthetic construct

<400> 14
Met Cys Leu Gly Arg Met Gly Ala Ser Ser Pro Arg Ser Pro Glu Pro
1   5   10   15
Val Gly Pro Pro Ala Pro Gly Leu Pro Phe Cys Cys Gly Gly Ser Leu
            20   25   30

11

```
Leu Ala Val Val Val Leu Leu Ala Leu Pro Val Ala Trp Gly Gln Cys
        35                      40                      45
Asn Ala Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr
        50                      55                      60
Asn Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr
65                      70                      75                      80
Glu Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu
                85                      90                      95
Lys Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser
                100                     105                     110
Cys Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys
        115                     120                     125
Gly Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr
        130                     135                     140
Arg Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr
145                     150                     155                     160
Val Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly
                165                     170                     175
Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu
                180                     185                     190
Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser
        195                     200                     205
Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys
        210                     215                     220
Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln
225                     230                     235                     240
Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile
                245                     250                     255
Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu
                260                     265                     270
Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys
        275                     280                     285
Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg
        290                     295                     300
Val Cys Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg
305                     310                     315                     320
Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu
                325                     330                     335
Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln
                340                     345                     350
Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp
        355                     360                     365
Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn
        370                     375                     380
Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
385                     390                     395                     400
Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
                405                     410                     415
Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
                420                     425                     430
Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
        435                     440                     445
Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
        450                     455                     460
Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
465                     470                     475                     480
Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
                485                     490                     495
Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
        500                     505                     510
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Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
        515                 520                 525
Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
        530                 535                 540
Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
545                 550                 555                 560
Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
                565                 570                 575
Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
                580                 585                 590
Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
        595                 600                 605
Asn Ala Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro
        610                 615                 620
Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn
625                 630                 635                 640
Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro
                645                 650                 655
Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
                660                 665                 670
Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
        675                 680                 685
Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
        690                 695                 700
Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val
705                 710                 715                 720
Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg
                725                 730                 735
Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
        740                 745                 750
Ser Arg Val Cys Gln Pro Pro Asp Val Leu His Ala Glu Arg Thr
        755                 760                 765
Gln Arg Asp Lys Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser
        770                 775                 780
Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr
785                 790                 795                 800
Pro Gln Gly Asp Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser
                805                 810                 815
Cys Asp Asp Phe Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro
                820                 825                 830
Val Asn Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly
        835                 840                 845
Phe Gln Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met
        850                 855                 860
Glu Ser Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys
865                 870                 875                 880
Pro Ser Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu
                885                 890                 895
Glu Val Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His
                900                 905                 910
Pro Asp Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg
        915                 920                 925
Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
        930                 935                 940
Arg Cys Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe
945                 950                 955                 960
Ala Lys Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr
                965                 970                 975
Ser Leu Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser
        980                 985                 990
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Ile Thr Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys
    995               1000              1005
Lys Arg Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val
    1010              1015              1020
His Val Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys
1025              1030              1035              1040
Thr Thr Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu
              1045              1050              1055
Ser Gly Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg
              1060              1065              1070
Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser
              1075              1080              1085
Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys
    1090              1095              1100
Asn Leu Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro
1105              1110              1115              1120
Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly
              1125              1130              1135
Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val
              1140              1145              1150
Glu Asn Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn
    1155              1160              1165
Glu Val Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro
    1170              1175              1180
Arg Arg Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro
1185              1190              1195              1200
Ser Cys Ser Arg Val Cys Gln Pro Pro Glu Ile Leu His Gly Glu
              1205              1210              1215
His Thr Pro Ser His Gln Asp Asn Phe Ser Pro Gly Gln Glu Val Phe
              1220              1225              1230
Tyr Ser Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His
              1235              1240              1245
Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val
    1250              1255              1260
Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu
1265              1270              1275              1280
Phe Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp
              1285              1290              1295
Glu Gly Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val
              1300              1305              1310
Gly Met Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile
    1315              1320              1325
Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr
    1330              1335              1340
Pro Ser Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp
1345              1350              1355              1360
Pro His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr
              1365              1370              1375
Ile Arg Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro
    1380              1385              1390
Ala Pro Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro
    1395              1400              1405
Glu Gln Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu
    1410              1415              1420
Phe Pro Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe
1425              1430              1435              1440
Gly Lys Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser
              1445              1450              1455
Val Glu Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Pro Glu Pro
    1460              1465              1470
```

14

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Phe Asn Gly Met Val His Ile Asn Thr Asp Thr Gln Phe Gly Ser Thr
        1475                1480                1485
Val Asn Tyr Ser Cys Asn Glu Gly Phe Arg Leu Ile Gly Ser Pro Ser
        1490                1495                1500
Thr Thr Cys Leu Val Ser Gly Asn Asn Val Thr Trp Asp Lys Lys Ala
1505                1510                1515                1520
Pro Ile Cys Glu Ile Ile Ser Cys Glu Pro Pro Thr Ile Ser Asn
        1525                1530                1535
Gly Asp Phe Tyr Ser Asn Asn Arg Thr Ser Phe His Asn Gly Thr Val
        1540                1545                1550
Val Thr Tyr Gln Cys His Thr Gly Pro Asp Gly Glu Gln Leu Phe Glu
        1555                1560                1565
Leu Val Gly Glu Arg Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val
        1570                1575                1580
Gly Val Trp Ser Ser Pro Pro Pro Arg Cys Ile Ser Thr Asn Lys Cys
1585                1590                1595                1600
Thr Ala Pro Glu Val Glu Asn Ala Ile Arg Val Pro Gly Asn Arg Ser
        1605                1610                1615
Phe Phe Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln Pro Gly Phe
        1620                1625                1630
Val Met Val Gly Ser His Thr Val Gln Cys Gln Thr Asn Gly Arg Trp
        1635                1640                1645
Gly Pro Lys Leu Pro His Cys Ser Arg Val Cys Gln Pro Pro Pro Glu
        1650                1655                1660
Ile Leu His Gly Glu His Thr Leu Ser His Gln Asp Asn Phe Ser Pro
1665                1670                1675                1680
Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Ser Tyr Asp Leu Arg Gly
        1685                1690                1695
Ala Ala Ser Leu His Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala
        1700                1705                1710
Pro Arg Cys Thr Val Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro
        1715                1720                1725
His Gly Arg Val Leu Leu Pro Leu Asn Leu Gln Leu Gly Ala Lys Val
        1730                1735                1740
Ser Phe Val Cys Asp Glu Gly Phe Arg Leu Lys Gly Arg Ser Ala Ser
1745                1750                1755                1760
His Cys Val Leu Ala Gly Met Lys Ala Leu Trp Asn Ser Ser Val Pro
        1765                1770                1775
Val Cys Glu Gln Ile Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly
        1780                1785                1790
Arg His Thr Gly Thr Pro Phe Gly Asp Ile Pro Tyr Gly Lys Glu Ile
        1795                1800                1805
Ser Tyr Ala Cys Asp Thr His Pro Asp Arg Gly Met Thr Phe Asn Leu
1810                1815                1820
Ile Gly Glu Ser Ser Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly
1825                1830                1835                1840
Val Trp Ser Ser Pro Ala Pro Arg Cys Glu Leu Ser Val Pro Ala Ala
        1845                1850                1855
Cys Pro His Pro Pro Lys Ile Gln Asn Gly His Tyr Ile Gly Gly His
        1860                1865                1870
Val Ser Leu Tyr Leu Pro Gly Met Thr Ile Ser Tyr Thr Cys Asp Pro
        1875                1880                1885
Gly Tyr Leu Leu Val Gly Lys Gly Phe Ile Phe Cys Thr Asp Gln Gly
        1890                1895                1900
Ile Trp Ser Gln Leu Asp His Tyr Cys Lys Glu Val Asn Cys Ser Phe
1905                1910                1915                1920
Pro Leu Phe Met Asn Gly Ile Ser Lys Glu Leu Glu Met Lys Lys Val
        1925                1930                1935
Tyr His Tyr Gly Asp Tyr Val Thr Leu Lys Cys Glu Asp Gly Tyr Thr
        1940                1945                1950
```

15

```
Leu Glu Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp
        1955            1960            1965
Pro Pro Leu Ala Lys Cys Thr Ser Arg Ala His Asp Ala Leu Ile Val
        1970            1975            1980
Gly Thr Leu Ser Gly Thr Ile Phe Phe Ile Leu Leu Ile Ile Phe Leu
1985            1990            1995            2000
Ser Trp Ile Ile Leu Lys His Arg Lys Gly Asn Asn Ala His Glu Asn
            2005            2010            2015
Pro Lys Glu Val Ala Ile His Leu His Ser Gln Gly Gly Ser Ser Val
        2020            2025            2030
His Pro Arg Thr Leu Gln Thr Asn Glu Glu Asn Ser Arg Val Leu Pro
        2035            2040            2045
```

<210> 15
<211> 1029
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
     synthetic construct

<400> 15
```
tgtgaggagc caccaacatt tgaagctatg gagctcattg gtaaaccaaa accctactat 60
gagattggtg aacgagtaga ttataagtgt aaaaaaggat acttctatat acctcctctt 120
gccacccata ctatttgtga tcggaatcat acatggctac ctgtctcaga tgacgcctgt 180
tatagagaaa catgtccata tacgggat cctttaaatg gccaagcagt ccctgcaaat 240
gggacttacg agtttggtta tcagatgcac tttatttgta atgagggtta ttacttaatt 300
ggtgaagaaa ttctatattg tgaacttaaa ggatcagtag caatttggag cggtaagccc 360
ccaatatgtg aaaaggtttt gtgtacacca cctccaaaaa taaaaaatgg aaaacacacc 420
tttagtgaag tagaagtatt tgagtatctt gatgcagtaa cttatagttg tgatcctgca 480
cctggaccag atccattttc acttattgga gagagcacga tttattgtgg tgacaattca 540
gtgtggagtc gtgctgctcc agagtgtaaa gtggtcaaat gtcgatttcc agtagtcgaa 600
aatggaaaac agatatcagg atttggaaaa aaattttact acaaagcaac agttatgttt 660
gaatgcgata agggtttta cctcgatggc agcgacacaa ttgtctgtga cagtaacagt 720
acttgggatc ccccagttcc aaagtgtctt aaagtgtcga cttcttccac tacaaaatct 780
ccagcgtcca gtgcctcagg tcctaggcct acttacaagc ctccagtctc aaattatcca 840
ggatatccta aacctgagga aggaatactt gacagtttgg atgtttgggt cattgctgtg 900
attgttattg ccatagttgt tggagttgca gtaatttgtg ttgtcccgta cagatatctt 960
caaaggagga agaagaagg cacataccta actgatgaga cccacagaga agtaaaattt 1020
acttctctc                                                       1029
```

<210> 16
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
     synthetic construct

<400> 16
```
Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
1               5               10              15
Phe Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe
            20              25              30
Ser Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile
        35              40              45
Gly Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys
    50              55              60
```

```
Cys Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile
65              70              75                      80
Cys Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr
                85              90                      95
Arg Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val
            100             105             110
Pro Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys
        115             120             125
Asn Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu
    130             135             140
Lys Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys
145             150             155                     160
Val Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe
            165             170             175
Ser Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys
        180             185             190
Asp Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr
    195             200             205
Ile Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys
    210             215             220
Lys Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile
225             230             235                     240
Ser Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu
            245             250             255
Cys Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp
            260             265             270
Ser Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser
    275             280             285
Thr Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg
    290             295             300
Pro Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro
305             310             315                     320
Glu Glu Gly Ile Leu Asp Ser Leu Asp Val Trp Val Ile Ala Val Ile
            325             330             335
Val Ile Ala Ile Val Val Gly Val Ala Val Ile Cys Val Val Pro Tyr
            340             345             350
Arg Tyr Leu Gln Arg Arg Lys Lys Lys Gly Thr Tyr Leu Thr Asp Glu
    355             360                     365
Thr His Arg Glu Val Lys Phe Thr Ser Leu
    370             375
```

```
<210> 17
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 17
Met Glu Val Ser Ser Arg Ser Ser Glu Pro Leu Asp Pro Val Trp Leu
1               5               10              15
Leu Val Ala Phe Gly Arg Gly Gly Val Lys Leu Glu Val Leu Leu Leu
            20              25              30
Phe Leu Leu Pro Phe Thr Leu Gly His Cys Pro Ala Pro Ser Gln Leu
        35              40              45
Pro Ser Ala Lys Pro Ile Asn Leu Thr Asp Glu Ser Met Phe Pro Ile
    50              55              60
```

```
Gly Thr Tyr Leu Leu Tyr Glu Cys Leu Pro Gly Tyr Ile Lys Arg Gln
65              70                  75                  80
Phe Ser Ile Thr Cys Lys Gln Asp Ser Thr Trp Thr Ser Ala Glu Asp
                85                  90                  95
Lys Cys Ile Arg Lys Gln Cys Lys Thr Pro Ser Asp Pro Glu Asn Gly
            100                 105                 110
Leu Val His Val His Thr Gly Ile Gln Phe Gly Ser Arg Ile Asn Tyr
        115                 120                 125
Thr Cys Asn Gln Gly Tyr Arg Leu Ile Gly Ser Ser Ser Ala Val Cys
    130                 135                 140
Val Ile Thr Asp Gln Ser Val Asp Trp Asp Thr Glu Ala Pro Ile Cys
145                 150                 155                 160
Glu Trp Ile Pro Cys Glu Ile Pro Pro Gly Ile Pro Asn Gly Asp Phe
                165                 170                 175
Phe Ser Ser Thr Arg Glu Asp Phe His Tyr Gly Met Val Val Thr Tyr
                180                 185                 190
Arg Cys Asn Thr Asp Ala Arg Gly Lys Ala Leu Phe Asn Leu Val Gly
            195                 200                 205
Glu Pro Ser Leu Tyr Cys Thr Ser Asn Asp Gly Glu Ile Gly Val Trp
    210                 215                 220
Ser Gly Pro Pro Pro Gln Cys Ile Glu Leu Asn Lys Cys Thr Pro Pro
225                 230                 235                 240
Pro Tyr Val Glu Asn Ala Val Met Leu Ser Glu Asn Arg Ser Leu Phe
                245                 250                 255
Ser Leu Arg Asp Ile Val Glu Phe Arg Cys His Pro Gly Phe Ile Met
            260                 265                 270
Lys Gly Ala Ser Ser Val His Cys Gln Ser Leu Asn Lys Trp Glu Pro
            275                 280                 285
Glu Leu Pro Ser Cys Phe Lys Gly Val Ile Cys Arg Leu Pro Gln Glu
    290                 295                 300
Met Ser Gly Phe Gln Lys Gly Leu Gly Met Lys Lys Glu Tyr Tyr Tyr
305                 310                 315                 320
Gly Glu Asn Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly
                325                 330                 335
Ser Ser Gln Ser Gln Cys Gln Ser Asp Gly Ser Trp Asn Pro Leu Leu
    340                 345                 350
Ala Lys Cys Val Ser Arg Ser Ile Ser Gly Leu Ile Val Gly Ile Phe
    355                 360                 365
Ile Gly Ile Ile Val Phe Ile Leu Val Ile Ile Val Phe Ile Trp Met
370                 375                 380
Ile Leu Lys Tyr Lys Lys Arg Asn Thr Thr Asp Glu Lys Tyr Lys Glu
385                 390                 395                 400
Val Gly Ile His Leu Asn Tyr Lys Glu Asp Ser Cys Val Arg Leu Gln
            405                 410                 415
Ser Leu Leu Thr Ser Gln Glu Asn Ser Ser Thr Thr Ser Pro Ala Arg
            420                 425                 430
Asn Ser Leu Thr Gln Glu Val Ser
            435                 440
```

<210> 18
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 18

```
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1               5                   10                  15
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            20                  25                  30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        35                  40                  45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
    50                  55                  60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
            85                  90                  95
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
            115                 120                 125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    130                 135                 140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145                 150                 155                 160
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
            165                 170                 175
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Pro Phe Phe Leu Tyr
            180                 185                 190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
            195                 200                 205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
            210                 215                 220
Ser Leu Ser Leu Ser Pro Gly Lys
225                 230
```

```
<210> 19
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 19
Gly Ser Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn
1               5                   10                  15
Ser Pro Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp
            20                  25                  30
Phe Leu Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser
        35                  40                  45
Asp Ile Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys
    50                  55                  60
Tyr Ala Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln
65                  70                  75                  80
Gly Thr Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn
            85                  90                  95
Lys Glu Lys Asn Val Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys
            100                 105                 110
Val Ser Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg
    115                 120                 125
Ser Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln
    130                 135                 140
```

```
Ile Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val
145                     150                 155                 160
Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr
                165                 170                 175
Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser
                180                 185                 190
Gln Ser Met Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln
            195                 200                 205
Gln Asn Ala Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg
        210                 215                 220
Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser
225                 230                 235                 240
Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val
                245                 250                 255
Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr
                260                 265                 270
Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu
            275                 280                 285
Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys
        290                 295                 300
Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser
305                 310                 315                 320
Arg Pro Lys Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro
                325                 330                 335
Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys
            340                 345                 350
Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln
            355                 360                 365
Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met
    370                 375                 380
Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr
385                 390                 395                 400
Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val
                405                 410                 415
Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys
            420                 425                 430
Ser Thr Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp
        435                 440                 445
Thr Ala Gly Thr Cys Tyr
    450
```

```
<210> 20
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 20
atgggcgccg cgggcctgct cggggttttc ttggctctcg tcgcaccggg ggtcctcggg   60
atttcttgtg gctctcctcc gcctatccta aatggccgga ttagttatta ttctaccccc  120
attgctgttg gtaccgtgat aaggtacagt tgttcaggta ccttccgcct cattggagaa  180
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct  240
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac  300
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc  360
aacttctcca tgaacggaaa caagtctgtt tggtgtcaag caaataatat gtggggccg   420
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc  480
cacaatggac atcacacaag tgagaatgtt ggctccattg ctccaggatt gtctgtgact  540
```

```
tacagctgtg aatctggtta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 600
ggaaaatgga gtgctgtccc ccccacatgt gaagaggcac gctgtaaatc tctaggacga 660
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaacttt 720
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 780
cagggagttg cttggaccaa aatgccagta tgtgaagaaa ttttttgccc actgcggccg 840
cagtctagag acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 900
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 960
gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 1020
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 1080
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 1140
gagtacaagt gcaaggtctc caacaaagcc ctcccagtcc catcgagaa aaccatctcc 1200
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 1260
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 1320
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 1380
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcaggtgg 1440
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 1500
cagaagagcc tctccctgtc cccgggtaaa                                  1530
```

```
<210> 21
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 21
Met Gly Ala Ala Gly Leu Leu Gly Val Phe Leu Ala Leu Val Ala Pro
1               5                   10                  15
Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Ile Leu Asn Gly
            20                  25                  30
Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
        35                  40                  45
Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
    50                  55                  60
Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
65                  70                  75                  80
Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
                85                  90                  95
Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
            100                 105                 110
Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
        115                 120                 125
Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
    130                 135                 140
Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
145                 150                 155                 160
His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
                165                 170                 175
Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
            180                 185                 190
Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
        195                 200                 205
Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
    210                 215                 220
Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
225                 230                 235                 240
Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
                245                 250                 255
```

```
Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
        260                     265                 270
Glu Ile Phe Cys Pro Leu Arg Pro Gln Ser Arg Asp Lys Thr His Thr
        275                     280                 285
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        290                     295                 300
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
305                     310                 315                 320
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
                325                 330                 335
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                340                 345                 350
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            355                 360                 365
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        370                     375                 380
Lys Val Ser Asn Lys Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser
385                     390                 395                 400
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
                405                 410                 415
Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
            420                     425                 430
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            435                 440                 445
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        450                     455                 460
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
465                     470                 475                 480
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
                485                 490                 495
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                500                 505                 510


<210> 22
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 22
Glu Pro Arg Ile Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Cys Pro
1                   5                   10                  15
Pro Gly Asn Ile Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys
            20                  25                  30
Pro Lys Asp Ala Leu Met Ile Ser Leu Thr Pro Lys Val Thr Cys Val
            35                  40                  45
Val Val Asp Val Ser Glu Asp Asp Pro Asp Val His Val Ser Trp Phe
        50                  55                  60
Val Asp Asn Lys Glu Val His Thr Ala Trp Thr Gln Pro Arg Glu Ala
65                  70                  75                  80
Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Ala Leu Pro Ile Gln His
                    85                  90                  95
Gln Asp Trp Met Arg Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys
            100                 105                 110
Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Arg
        115                 120                     125
```

```
Ala Gln Thr Pro Gln Val Tyr Thr Ile Pro Pro Pro Arg Glu Gln Met
    130                 135             140
Ser Lys Lys Lys Val Ser Leu Thr Cys Leu Val Thr Asn Phe Phe Ser
145                 150                 155                 160
Glu Ala Ile Ser Val Glu Trp Glu Arg Asn Gly Glu Leu Glu Gln Asp
                165                 170                 175
Tyr Lys Asn Thr Pro Pro Ile Leu Asp Ser Asp Gly Thr Tyr Phe Leu
            180                 185                 190
Tyr Ser Lys Leu Thr Val Asp Thr Asp Ser Trp Leu Gln Gly Glu Ile
        195                 200                 205
Phe Thr Cys Ser Val Val His Glu Ala Leu His Asn His His Thr Gln
    210                 215                 220
Lys Asn Leu Ser Arg Ser Pro Gly Lys
225                 230
```

<210> 23
<211> 4860
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
     synthetic construct

<400> 23
```
gctctctaca ccctcatcac ccctgctgtt ttgcgaacag acacagaaga gcaaattttg 60
gtggaggccc atggagacag tactccaaaa cagcttgaca tctttgttca tgattttcca 120
cggaagcaga aaaccttgtt ccaaaccaga gtagatatga atccagcagg aggcatgctt 180
gtcactccaa ctatagagat tccagcaaaa gaagtgagta cggactccag gcaaaatcaa 240
tatgtggttg tgcaagtaac tggtcctcaa gtgagattgg aaaaggtggt tctcctttct 300
taccagagta gctttctgtt tatccagaca gataaaggca tctatacacc agggtctcca 360
gtactctatc gtgttttttc tatggatcac aacacaagca agatgaacaa aactgtgatt 420
gttgagtttc agactccaga aggcattctt gtcagttcta attcagttga cctaaacttc 480
ttctggcctt acaatttacc agaccttgtc agtttgggga cttggaggat tgtggccaaa 540
tatgaacatt ccccagagaa ttatactgca tattttgatg tcaggaaata tgtgttgcca 600
agctttgaag tccgtctgca accatcagag aagttttttt acattgacgg caatgaaaat 660
ttccacgtgt ctatcactgc aaggtacttg tatggagagg aagtggaagg tgtggccttt 720
gtcctctttg gagtgaaaat agatgatgct aaaaagagta ttccagactc actcacgaga 780
attccgatta ttgatggaga tgggaaagca acactaaaaa gagatacatt ccgttctcga 840
tttccaaatc tcaatgagct tgttgggcat actctgtatg catctgtaac agtcatgaca 900
gaatcaggca gtgatatggt agtgactgag caaagcggca ttcatattgt ggcatctccc 960
tatcagatcc acttcacaaa aacccccaaa tatttcaagc caggaatgcc atatgaactg 1020
acggtgtatg ttaccaaccc tgatggctca ccagctgccc atgtgccagt ggtatcagag 1080
gcctttcatt ctatgggaac cactttgagt gatgggactg ctaagctcat cctgaacata 1140
ccattgaatg ctcaaagcct accaatcact gttagaacta accatggaga cctcccaaga 1200
gaacgccagg caacaaagtc catgacagcc atagcctacc aaacccaggg aggatctgga 1260
aactatcttc atgtagccat tacatctaca gagattaagc ccggagataa cttacctgtc 1320
aatttcaatg tgaagggcaa tgcaaattca ctgaagcaga tcaaatattt cacatacctc 1380
atattgaata aagggaagat tttcaaggtt ggcaggcaac ccaggagaga tgggcagaat 1440
ctggtgacca tgaatctgca tatcactcca gatctcatcc cttccttccg gtttgtggct 1500
tactaccaag tgggaaacaa cgaaattgtg gctgattctg tctgggtgga gtgaaggat 1560
acctgcatgg gaacgttggt tgtgaaagga acaatctaa tacaaatgcc aggagctgca 1620
atgaaaatca aattggaagg ggatccaggt gctcgggttg gtcttgtggc gtgtggacaaa 1680
gcagtatatg ttctcaatga taaatataag attagccaag ctaagatatg ggacacaata 1740
gaaaagagtg actttggctg tacagctggc agtggccaga ataatctggg tgtgtttgaa 1800
gatgctggac tggctctgac aaccagcact aatctcaaca ccaaacagag atcagctgca 1860
aagtgtcctc agcctgcaaa tcggaggcgt cgcagttctg ttttgctgct tgacagcaac 1920
gcaagcaaag cggcagaatt tcaggatcaa gacctgcgta atgctgtga agatgtcatg 1980
catgagaacc ccatggggta cacttgtgaa aagcgtgcaa aatacatcca ggagggagat 2040
gcttgtaagg ctgccttcct tgaatgctgt cgctacatca aggggggtccg agatgaaaac 2100
```

```
caacgggaga gcgagttgtt tctggcaaga gatgataatg aagatggttt catagcagat 2160
agtgatatca tctcaaggtc tgatttcccc aagagttggt tgtggctaac aaaggacttg 2220
accgaggagc ctaacagtca agggatttca agcaagacaa tgtcttttta tctgagggat 2280
tccatcacaa cctgggtggt gctggctgta agctttacac ccaccaaagg gatctgtgtg 2340
gctgaacctt atgaaataag agtcatgaaa gtcttcttca ttgatcttca aatgccatat 2400
tcagtagtga agaatgagca ggtggagatt cgagctattc tgcacaacta cgttaacgag 2460
gatatttatg tgcgagtgga actgttatac aacccagcct ctgcagtgc ttccacaaaa 2520
ggacaaagat accgacagca gttcccaatt aaagccctgt cctccagagc agtaccgttt 2580
gtgatagtcc cattagagca aggattgcat gatgttgaga ttaaagcaag tgtccaggaa 2640
gcgttgtggt cagacggtgt gaggaagaaa ctgaaagttg tacctgaagg ggtacagaaa 2700
tccattgtga ctattgttaa actggaccca agggcaaaag gagttggtgg aacacagcta 2760
gaagtgatca aagcccgcaa attagatgac agagtgcctg acacagaaat tgaaaccaag 2820
attatcatcc aaggtgaccc tgtggctcag attattgaaa actcaattga tggaagtaaa 2880
ctcaaccatc tcattatcac tccttctggc tgtggggagc aaaatatgat ccgcatggcc 2940
gcaccagtta ttgccaccta ctacctggac accacagagc agtgggagac tctcggcata 3000
aatcgcagga ctgaagctgt caatcagatc gtgactggtt atgcccagca gatggtgtac 3060
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gcatatgtcg taaaagtctt tgccatggct gccaaaatgg tagcaggcat tagtcatgaa 3180
atcatttgtg gaggtgtgag gtggctgatt ctgaacaggc aacaaccaga tggagcgttc 3240
aaagaaaatg cccctgtact ttctggaaca atgcagggag gaattcaagg tgctgaagaa 3300
gaagtatatt taacagcttt cattctggtt gcgttgttgg aatccaaaac aatctgcaat 3360
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tatgagaaac tgcaaaggcc ttacactaca gccctacag cctatgcttt ggctgctgca 3480
gaccaactca atgatgacag ggtactcatg gcagcatcaa caggaaggga tcattgggaa 3540
gaatacaatg ctcacaccca caacattgaa ggcacttcct atgccttgtt ggccctgctg 3600
aaaatgaaga aatttgatca aactggtccc atagtcagat ggctgacaga tcagaatttt 3660
tatgggaaa catatggaca aacccaagca acagttatgg catttcaagc tcttgctgaa 3720
tatgagattc agatgcctac ccataaggac ttaaacttag atattactat tgaactgcca 3780
gatcgagaag tacctataag gtacagaatt aattatgaaa atgctctcct ggctcggaca 3840
gtagagacca aactcaacca agacatcact gtgacagcat caggtgatgg aaaagcaaca 3900
atgaccattt tgacattcta taacgcacag ttgcaggaga aggcaaatgt ttgcaataaa 3960
tttcatctta atgtttctgt tgaaaacatc cacttgaatg caatgggagc caagggagcc 4020
ctcatgctca agatctgcac aaggtatctg ggagaagttg attctacaat gacaataatt 4080
gatatttcta tgctgactgg ttttctccct gatgctgaag accttacaag gctttctaaa 4140
ggagtggaca gatacatctc cagatatgaa gttgacaata atatggctca gaaagtagct 4200
gttatcattt acttaaacaa ggtctcccac tctgaagatg aatgcctgca ctttaagatt 4260
ctcaagcatt ttgaagttgg cttcattcag ccaggatcag tcaaggtgta cagctactac 4320
aatctagatg aaaaatgtac caagttctac catccagata aaggaacagg ccttctcaat 4380
aagatatgta ttggtaacgt ttgccgatgt gcaggagaaa cctgttcctc gctcaaccat 4440
caggaaagga ttgatgttcc attacaaatt gaaaaagcct gcgagacgaa tgtggattat 4500
gtctacaaaa ccaagctgct tcgaatagaa gaacaagatg gtaatgatat ctatgtcatg 4560
gatgttttag aagttattaa acaaggtact gacgaaaatc cacgagcaaa gacccaccag 4620
tacataagtc aaaggaaatg ccaggaggct ctgaatctga aggtgaatga tgattatctg 4680
atctggggtt ccaggagtga cctgttgccc acgaaagata aaatttccta catcattaca 4740
aagaacacat ggattgagag atggccacat gaagacgaat gtcaggaaga agaattccaa 4800
aagttgtgtg atgactttgc tcagtttagc tacacattga ctgagtttgg ctgccctact 4860
```

```
<210>  24
<211>  1620
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Description of Artificial Sequence:/note =
       synthetic construct

<400>  24
Ala Leu Tyr Thr Leu Ile Thr Pro Ala Val Leu Arg Thr Asp Thr Glu
 1               5                   10                  15
```

```
Glu Gln Ile Leu Val Glu Ala His Gly Asp Ser Thr Pro Lys Gln Leu
          20                      25                      30
Asp Ile Phe Val His Asp Phe Pro Arg Lys Gln Lys Thr Leu Phe Gln
          35                      40                      45
Thr Arg Val Asp Met Asn Pro Ala Gly Gly Met Leu Val Thr Pro Thr
    50                      55                      60
Ile Glu Ile Pro Ala Lys Glu Val Ser Thr Asp Ser Arg Gln Asn Gln
65                      70                      75                      80
Tyr Val Val Val Gln Val Thr Gly Pro Gln Val Arg Leu Glu Lys Val
                85                      90                      95
Val Leu Leu Ser Tyr Gln Ser Ser Phe Leu Phe Ile Gln Thr Asp Lys
              100                     105                     110
Gly Ile Tyr Thr Pro Gly Ser Pro Val Leu Tyr Arg Val Phe Ser Met
          115                     120                     125
Asp His Asn Thr Ser Lys Met Asn Lys Thr Val Ile Val Glu Phe Gln
    130                     135                     140
Thr Pro Glu Gly Ile Leu Val Ser Ser Asn Ser Val Asp Leu Asn Phe
145                     150                     155                     160
Phe Trp Pro Tyr Asn Leu Pro Asp Leu Val Ser Leu Gly Thr Trp Arg
                165                     170                     175
Ile Val Ala Lys Tyr Glu His Ser Pro Glu Asn Tyr Thr Ala Tyr Phe
              180                     185                     190
Asp Val Arg Lys Tyr Val Leu Pro Ser Phe Glu Val Arg Leu Gln Pro
          195                     200                     205
Ser Glu Lys Phe Phe Tyr Ile Asp Gly Asn Glu Asn Phe His Val Ser
    210                     215                     220
Ile Thr Ala Arg Tyr Leu Tyr Gly Glu Glu Val Glu Gly Val Ala Phe
225                     230                     235                     240
Val Leu Phe Gly Val Lys Ile Asp Asp Ala Lys Lys Ser Ile Pro Asp
              245                     250                     255
Ser Leu Thr Arg Ile Pro Ile Ile Asp Gly Asp Gly Lys Ala Thr Leu
          260                     265                     270
Lys Arg Asp Thr Phe Arg Ser Arg Phe Pro Asn Leu Asn Glu Leu Val
          275                     280                     285
Gly His Thr Leu Tyr Ala Ser Val Thr Val Met Thr Glu Ser Gly Ser
    290                     295                     300
Asp Met Val Val Thr Glu Gln Ser Gly Ile His Ile Val Ala Ser Pro
305                     310                     315                     320
Tyr Gln Ile His Phe Thr Lys Thr Pro Lys Tyr Phe Lys Pro Gly Met
              325                     330                     335
Pro Tyr Glu Leu Thr Val Tyr Val Thr Asn Pro Asp Gly Ser Pro Ala
          340                     345                     350
Ala His Val Pro Val Val Ser Glu Ala Phe His Ser Met Gly Thr Thr
          355                     360                     365
Leu Ser Asp Gly Thr Ala Lys Leu Ile Leu Asn Ile Pro Leu Asn Ala
    370                     375                     380
Gln Ser Leu Pro Ile Thr Val Arg Thr Asn His Gly Asp Leu Pro Arg
385                     390                     395                     400
Glu Arg Gln Ala Thr Lys Ser Met Thr Ala Ile Ala Tyr Gln Thr Gln
              405                     410                     415
Gly Gly Ser Gly Asn Tyr Leu His Val Ala Ile Thr Ser Thr Glu Ile
          420                     425                     430
Lys Pro Gly Asp Asn Leu Pro Val Asn Phe Asn Val Lys Gly Asn Ala
          435                     440                     445
Asn Ser Leu Lys Gln Ile Lys Tyr Phe Thr Tyr Leu Ile Leu Asn Lys
    450                     455                     460
Gly Lys Ile Phe Lys Val Gly Arg Gln Pro Arg Arg Asp Gly Gln Asn
465                     470                     475                     480
Leu Val Thr Met Asn Leu His Ile Thr Pro Asp Leu Ile Pro Ser Phe
              485                     490                     495
```

25

```
Arg Phe Val Ala Tyr Tyr Gln Val Gly Asn Asn Glu Ile Val Ala Asp
        500                     505                 510
Ser Val Trp Val Asp Val Lys Asp Thr Cys Met Gly Thr Leu Val Val
        515                     520                 525
Lys Gly Asp Asn Leu Ile Gln Met Pro Gly Ala Ala Met Lys Ile Lys
    530                     535                 540
Leu Glu Gly Asp Pro Gly Ala Arg Val Gly Leu Val Ala Val Asp Lys
545                     550                 555                 560
Ala Val Tyr Val Leu Asn Asp Lys Tyr Lys Ile Ser Gln Ala Lys Ile
            565                     570                 575
Trp Asp Thr Ile Glu Lys Ser Asp Phe Gly Cys Thr Ala Gly Ser Gly
            580                     585                 590
Gln Asn Asn Leu Gly Val Phe Glu Asp Ala Gly Leu Ala Leu Thr Thr
        595                     600                 605
Ser Thr Asn Leu Asn Thr Lys Gln Arg Ser Ala Ala Lys Cys Pro Gln
    610                     615                 620
Pro Ala Asn Arg Arg Arg Arg Ser Ser Val Leu Leu Leu Asp Ser Asn
625                     630                 635                 640
Ala Ser Lys Ala Ala Glu Phe Gln Asp Gln Asp Leu Arg Lys Cys Cys
            645                     650                 655
Glu Asp Val Met His Glu Asn Pro Met Gly Tyr Thr Cys Glu Lys Arg
            660                     665                 670
Ala Lys Tyr Ile Gln Glu Gly Asp Ala Cys Lys Ala Ala Phe Leu Glu
        675                     680                 685
Cys Cys Arg Tyr Ile Lys Gly Val Arg Asp Glu Asn Gln Arg Glu Ser
    690                     695                 700
Glu Leu Phe Leu Ala Arg Asp Asp Asn Glu Asp Gly Phe Ile Ala Asp
705                     710                 715                 720
Ser Asp Ile Ile Ser Arg Ser Asp Phe Pro Lys Ser Trp Leu Trp Leu
            725                     730                 735
Thr Lys Asp Leu Thr Glu Glu Pro Asn Ser Gln Gly Ile Ser Ser Lys
        740                     745                 750
Thr Met Ser Phe Tyr Leu Arg Asp Ser Ile Thr Thr Trp Val Val Leu
        755                     760                 765
Ala Val Ser Phe Thr Pro Thr Lys Gly Ile Cys Val Ala Glu Pro Tyr
    770                     775                 780
Glu Ile Arg Val Met Lys Val Phe Phe Ile Asp Leu Gln Met Pro Tyr
785                     790                 795                 800
Ser Val Val Lys Asn Glu Gln Val Glu Ile Arg Ala Ile Leu His Asn
            805                     810                 815
Tyr Val Asn Glu Asp Ile Tyr Val Arg Val Glu Leu Leu Tyr Asn Pro
        820                     825                 830
Ala Phe Cys Ser Ala Ser Thr Lys Gly Gln Arg Tyr Arg Gln Gln Phe
        835                     840                 845
Pro Ile Lys Ala Leu Ser Ser Arg Ala Val Pro Phe Val Ile Val Pro
    850                     855                 860
Leu Glu Gln Gly Leu His Asp Val Glu Ile Lys Ala Ser Val Gln Glu
865                     870                 875                 880
Ala Leu Trp Ser Asp Gly Val Arg Lys Lys Leu Lys Val Val Pro Glu
            885                     890                 895
Gly Val Gln Lys Ser Ile Val Thr Ile Val Lys Leu Asp Pro Arg Ala
            900                     905                 910
Lys Gly Val Gly Gly Thr Gln Leu Glu Val Ile Lys Ala Arg Lys Leu
        915                     920                 925
Asp Asp Arg Val Pro Asp Thr Glu Ile Glu Thr Lys Ile Ile Ile Gln
    930                     935                 940
Gly Asp Pro Val Ala Gln Ile Ile Glu Asn Ser Ile Asp Gly Ser Lys
945                     950                 955                 960
Leu Asn His Leu Ile Ile Thr Pro Ser Gly Cys Gly Glu Gln Asn Met
            965                     970                 975
```

```
Ile Arg Met Ala Ala Pro Val Ile Ala Thr Tyr Tyr Leu Asp Thr Thr
          980                 985                 990
Glu Gln Trp Glu Thr Leu Gly Ile Asn Arg Arg Thr Glu Ala Val Asn
          995                1000                1005
Gln Ile Val Thr Gly Tyr Ala Gln Gln Met Val Tyr Lys Lys Ala Asp
     1010                1015                1020
His Ser Tyr Ala Ala Phe Thr Asn Arg Ala Ser Ser Ser Trp Leu Thr
1025                1030                1035                1040
Ala Tyr Val Val Lys Val Phe Ala Met Ala Ala Lys Met Val Ala Gly
               1045                1050                1055
Ile Ser His Glu Ile Ile Cys Gly Gly Val Arg Trp Leu Ile Leu Asn
               1060                1065                1070
Arg Gln Gln Pro Asp Gly Ala Phe Lys Glu Asn Ala Pro Val Leu Ser
          1075                1080                1085
Gly Thr Met Gln Gly Gly Ile Gln Gly Ala Glu Glu Glu Val Tyr Leu
          1090                1095                1100
Thr Ala Phe Ile Leu Val Ala Leu Leu Glu Ser Lys Thr Ile Cys Asn
1105                1110                1115                1120
Asp Tyr Val Asn Ser Leu Asp Ser Ser Ile Lys Lys Ala Thr Asn Tyr
               1125                1130                1135
Leu Leu Lys Lys Tyr Glu Lys Leu Gln Arg Pro Tyr Thr Thr Ala Leu
          1140                1145                1150
Thr Ala Tyr Ala Leu Ala Ala Ala Asp Gln Leu Asn Asp Asp Arg Val
          1155                1160                1165
Leu Met Ala Ala Ser Thr Gly Arg Asp His Trp Glu Glu Tyr Asn Ala
     1170                1175                1180
His Thr His Asn Ile Glu Gly Thr Ser Tyr Ala Leu Leu Ala Leu Leu
1185                1190                1195                1200
Lys Met Lys Lys Phe Asp Gln Thr Gly Pro Ile Val Arg Trp Leu Thr
          1205                1210                1215
Asp Gln Asn Phe Tyr Gly Glu Thr Tyr Gly Gln Thr Gln Ala Thr Val
          1220                1225                1230
Met Ala Phe Gln Ala Leu Ala Glu Tyr Glu Ile Gln Met Pro Thr His
          1235                1240                1245
Lys Asp Leu Asn Leu Asp Ile Thr Ile Glu Leu Pro Asp Arg Glu Val
     1250                1255                1260
Pro Ile Arg Tyr Arg Ile Asn Tyr Glu Asn Ala Leu Leu Ala Arg Thr
1265                1270                1275                1280
Val Glu Thr Lys Leu Asn Gln Asp Ile Thr Val Thr Ala Ser Gly Asp
          1285                1290                1295
Gly Lys Ala Thr Met Thr Ile Leu Thr Phe Tyr Asn Ala Gln Leu Gln
          1300                1305                1310
Glu Lys Ala Asn Val Cys Asn Lys Phe His Leu Asn Val Ser Val Glu
     1315                1320                1325
Asn Ile His Leu Asn Ala Met Gly Ala Lys Gly Ala Leu Met Leu Lys
     1330                1335                1340
Ile Cys Thr Arg Tyr Leu Gly Glu Val Asp Ser Thr Met Thr Ile Ile
1345                1350                1355                1360
Asp Ile Ser Met Leu Thr Gly Phe Leu Pro Asp Ala Glu Asp Leu Thr
               1365                1370                1375
Arg Leu Ser Lys Gly Val Asp Arg Tyr Ile Ser Arg Tyr Glu Val Asp
          1380                1385                1390
Asn Asn Met Ala Gln Lys Val Ala Val Ile Ile Tyr Leu Asn Lys Val
     1395                1400                1405
Ser His Ser Glu Asp Glu Cys Leu His Phe Lys Ile Leu Lys His Phe
     1410                1415                1420
Glu Val Gly Phe Ile Gln Pro Gly Ser Val Lys Val Tyr Ser Tyr Tyr
1425                1430                1435                1440
Asn Leu Asp Glu Lys Cys Thr Lys Phe Tyr His Pro Asp Lys Gly Thr
               1445                1450                1455
```

```
Gly Leu Leu Asn Lys Ile Cys Ile Gly Asn Val Cys Arg Cys Ala Gly
          1460              1465              1470
Glu Thr Cys Ser Ser Leu Asn His Gln Glu Arg Ile Asp Val Pro Leu
      1475              1480              1485
Gln Ile Glu Lys Ala Cys Glu Thr Asn Val Asp Tyr Val Tyr Lys Thr
      1490              1495              1500
Lys Leu Leu Arg Ile Glu Glu Gln Asp Gly Asn Asp Ile Tyr Val Met
1505              1510              1515              1520
Asp Val Leu Glu Val Ile Lys Gln Gly Thr Asp Glu Asn Pro Arg Ala
              1525              1530              1535
Lys Thr His Gln Tyr Ile Ser Gln Arg Lys Cys Gln Glu Ala Leu Asn
          1540              1545              1550
Leu Lys Val Asn Asp Asp Tyr Leu Ile Trp Gly Ser Arg Ser Asp Leu
          1555              1560              1565
Leu Pro Thr Lys Asp Lys Ile Ser Tyr Ile Ile Thr Lys Asn Thr Trp
      1570              1575              1580
Ile Glu Arg Trp Pro His Glu Asp Glu Cys Gln Glu Glu Glu Phe Gln
1585              1590              1595              1600
Lys Leu Cys Asp Asp Phe Ala Gln Phe Ser Tyr Thr Leu Thr Glu Phe
              1605              1610              1615
Gly Cys Pro Thr
          1620
```

```
<210> 25
<211> 3039
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 25
atttcttgtg gctctcctcc gcctatccta aatggccgga ttagttatta ttctacccCc 60
attgctgttg gtaccgtgat aaggtacagt tgttcaggta ccttccgcct cattggagaa 120
aaaagtctat tatgcataac taaagacaaa gtggatggaa cctgggataa acctgctcct 180
aaatgtgaat atttcaataa atattcttct tgccctgagc ccatagtacc aggaggatac 240
aaaattagag gctctacacc ctacagacat ggtgattctg tgacatttgc ctgtaaaacc 300
aacttctcca tgaacggaaa caagtctgtt tggtgtcaag caaataatat gtgggggccg 360
acacgactac caacctgtgt aagtgttttc cctctcgagt gtccagcact tcctatgatc 420
cacaatggac atcacacaag tgagaatgtt ggctccattg ctccaggatt gtctgtgact 480
tacagctgtg aatctggtta cttgcttgtt ggagaaaaga tcattaactg tttgtcttcg 540
ggaaaatgga gtgctgtccc ccccacatgt gaagaggcac gctgtaaatc tctaggacga 600
tttcccaatg ggaaggtaaa ggagcctcca attctccggg ttggtgtaac tgcaaacttt 660
ttctgtgatg aagggtatcg actgcaaggc ccaccttcta gtcggtgtgt aattgctgga 720
cagggagttg cttggaccaa aatgccagta tgtgaagaaa tttttgccc atcacctccc 780
cctattctca atggaagaca tataggcaac tcactagcaa atgtctcata tggaagcata 840
gtcacttaca cttgtgaccc ggacccagag gaaggagtga acttcatcct tattggagag 900
agcactctcc gttgtacagt tgatagtcag aagactggga cctggagtgg ccctgcccca 960
cgctgtgaac tttctacttc tgcggttcag tgtccacatc cccagatcct aagaggccga 1020
atggtatctg gcagaaaga tcgatatacc tataacgaca ctgtgatatt tgcttgcatg 1080
tttggcttca ccttgaaggg cagcaagcaa atccgatgca atgcccaagg cacatgggag 1140
ccatctgcac cagtctgtga aaaggaatgc caggcccctc ctaacatcct caatgggcaa 1200
aaggaagata gacacatggt ccgctttgac cctggaacat ctataaaata tagctgtaac 1260
cctggctatg tgctggtggg agaagaatcc atacagtgta cctctgaggg ggtgtggaca 1320
cccctgtac cccaatgcaa agtggcagcg tgtgaagcta caggaaggca actcttgaca 1380
aaaccccagc accaatttgt tagaccagat gtcaactctt cttgtggtga agggtacaag 1440
ttaagtggga gtgtttatca ggagtgtcaa ggcacaattc cttggtttat ggagattcgt 1500
ctttgtaaag aaatcacctg cccaccaccc cctgttatct acaatggggc acacaccggg 1560
agttccttag aagattttcc atatggaacc acggtcactt acacatgtaa ccctgggcca 1620
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```

                                      28
```

```
gaaagaggag tggaattcag cctcattgga gagagcacca tccgttgtac aagcaatgat 1680
caagaaagag gcacctggag tggccctgct cccctatgta aactttccct ccttgctgtc 1740
cagtgctcac atgtccatat tgcaaatgga tacaagatat ctggcaagga agccccatat 1800
ttctacaatg acactgtgac attcaagtgt tatagtggat ttactttgaa gggcagtagt 1860
cagattcgtt gcaaagctga taacacctgg gatcctgaaa taccagtttg tgaaaaagaa 1920
acatgccagc atgtgagaca gagtcttcaa gaacttccag ctggttcacg tgtggagcta 1980
gttaatacgt cctgccaaga tgggtaccag ttgactggac atgcttatca gatgtgtcaa 2040
gatgctgaaa atggaatttg gttcaaaaag attccacttt gtaaagttat tcactgtcac 2100
cctccaccag tgattgtcaa tgggaagcac acagggatga tggcagaaaa ctttctatat 2160
ggaaatgaag tctcttatga atgtgaccaa ggattctatc tcctgggaga gaaaaaattg 2220
cagtgcagaa gtgattctaa aggacatgga tcttggagcg ggccttcccc acagtgctta 2280
cgatctcctc ctgtgactcg ctgccctaat ccagaagtca aacatgggta caagctcaat 2340
aaaacacatt ctgcatattc ccacaatgac atagtgtatg ttgactgcaa tcctggcttc 2400
atcatgaatg gtagtcgcgt gattaggtgt catactgata acacatgggt gccaggtgtg 2460
ccaacttgta tgaaaaaagc cttcataggg tgtccacctc cgcctaagac ccctaacggg 2520
aaccatactg gtggaaacat agctcgattt tctcctggaa tgtcaatcct gtacagctgt 2580
gaccaaggct acctgctggt gggagaggca ctccttcttt gcacacatga gggaacctgg 2640
agccaacctg cccctcattg taaagaggta aactgtagct caccagcaga tatggatgga 2700
atccagaaag gctggaacc aaggaaaatg tatcagtatg agctgttgt aactctggag 2760
tgtgaagatg ggtatatgct ggaaggcagt ccccagagcc agtgccaatc ggatcaccaa 2820
tggaaccctc ccctggcggt ttgcagatcc cgttcacttg ctcctgtcct ttgtggtatt 2880
gctgcaggtt tgatacttct taccttcttg attgtcatta ccttatacgt gatatcaaaa 2940
cacagagaac gcaattatta tacagataca agccagaaag aagcttttca tttagaagca 3000
cgagaagtat attctgttga tccatacaac ccagccagc                          3039
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<210> 26
<211> 1033
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 26

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Met Gly Ala Ala Gly Leu Leu Gly Val Phe Leu Ala Leu Val Ala Pro
 1               5                  10                  15
Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Ile Leu Asn Gly
            20                  25                  30
Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
        35                  40                  45
Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
    50                  55                  60
Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
65                  70                  75                  80
Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
                85                  90                  95
Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
            100                 105                 110
Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
        115                 120                 125
Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
    130                 135                 140
Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
145                 150                 155                 160
His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
                165                 170                 175
Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
            180                 185                 190
Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
        195                 200                 205
```

29

```
Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
210                     215             220
Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
225                 230             235                 240
Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
                245             250                 255
Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
            260             265                 270
Glu Ile Phe Cys Pro Ser Pro Pro Ile Leu Asn Gly Arg His Ile
        275             280             285
Gly Asn Ser Leu Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr
    290             295             300
Cys Asp Pro Asp Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu
305             310                 315                 320
Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser
            325             330                 335
Gly Pro Ala Pro Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro
        340             345                 350
His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg
        355             360                 365
Tyr Thr Tyr Asn Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr
370             375                 380
Leu Lys Gly Ser Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu
385             390                 395                 400
Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile
            405             410                 415
Leu Asn Gly Gln Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly
        420             425                 430
Thr Ser Ile Lys Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu
        435             440             445
Glu Ser Ile Gln Cys Thr Ser Glu Gly Val Trp Thr Pro Pro Val Pro
    450             455                 460
Gln Cys Lys Val Ala Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr
465             470                 475                 480
Lys Pro Gln His Gln Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly
            485             490                 495
Glu Gly Tyr Lys Leu Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr
        500             505             510
Ile Pro Trp Phe Met Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro
        515             520                 525
Pro Pro Pro Val Ile Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu
    530             535             540
Asp Phe Pro Tyr Gly Thr Thr Val Thr Tyr Thr Cys Asn Pro Gly Pro
545             550             555                 560
Glu Arg Gly Val Glu Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys
            565             570             575
Thr Ser Asn Asp Gln Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu
        580             585             590
Cys Lys Leu Ser Leu Leu Ala Val Gln Cys Ser His Val His Ile Ala
        595             600             605
Asn Gly Tyr Lys Ile Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp
    610             615             620
Thr Val Thr Phe Lys Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser
625             630             635                 640
Gln Ile Arg Cys Lys Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val
            645             650             655
Cys Glu Lys Glu Thr Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu
            660             665             670
Pro Ala Gly Ser Arg Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly
        675             680             685
```

```
Tyr Gln Leu Thr Gly His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn
    690                     695             700
Gly Ile Trp Phe Lys Lys Ile Pro Leu Cys Lys Val Ile His Cys His
705                 710                 715                 720
Pro Pro Pro Val Ile Val Asn Gly Lys His Thr Gly Met Met Ala Glu
                725                 730                 735
Asn Phe Leu Tyr Gly Asn Glu Val Ser Tyr Glu Cys Asp Gln Gly Phe
            740                 745                 750
Tyr Leu Leu Gly Glu Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly
        755                 760                 765
His Gly Ser Trp Ser Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro
    770                 775                 780
Val Thr Arg Cys Pro Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn
785                 790                 795                 800
Lys Thr His Ser Ala Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys
                805                 810                 815
Asn Pro Gly Phe Ile Met Asn Gly Ser Arg Val Ile Arg Cys His Thr
                820                 825                 830
Asp Asn Thr Trp Val Pro Gly Val Pro Thr Cys Met Lys Lys Ala Phe
        835                 840                 845
Ile Gly Cys Pro Pro Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly
    850                 855                 860
Gly Asn Ile Ala Arg Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys
865                 870                 875                 880
Asp Gln Gly Tyr Leu Leu Val Gly Glu Ala Leu Leu Leu Cys Thr His
            885                 890                 895
Glu Gly Thr Trp Ser Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys
            900                 905                 910
Ser Ser Pro Ala Asp Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg
        915                 920                 925
Lys Met Tyr Gln Tyr Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly
    930                 935                 940
Tyr Met Leu Glu Gly Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln
945                 950                 955                 960
Trp Asn Pro Pro Leu Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val
                965                 970                 975
Leu Cys Gly Ile Ala Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val
            980                 985                 990
Ile Thr Leu Tyr Val Ile Ser Lys His Arg Glu Arg Asn Tyr Tyr Thr
    995                 1000                1005
Asp Thr Ser Gln Lys Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr
    1010                1015                1020
Ser Val Asp Pro Tyr Asn Pro Ala Ser
1025                1030
```

```
<210> 27
<211> 3042
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 27
atttcttgtg accctcctcc tgaagtcaaa aatgctcgga aaccctatta ttctcttccc 60
atagttcctg gaactgttct gaggtacact tgttcaccta gctaccgcct cattggagaa 120
aaggctatct tttgtataag tgaaaatcaa gtgcatgcca cctgggataa agctcctcct 180
atatgtgaat ctgtgaataa aaccatttct tgctcagatc ccatagtacc aggggggattc 240
atgaataaag gatctaaggc accattcaga catggtgatt ctgtgacatt tacctgtaaa 300
```

31

```
gccaacttca ccatgaaagg aagcaaaact gtctggtgcc aggcaaatga aatgtgggga 360
ccaacagctc tgccagtctg tgagagtgat ttccctctgg agtgcccatc acttccaacg 420
attcataatg gacaccacac aggacagcat gttgaccagt ttgttgctgg gttgtctgtg 480
acatacagtt gtgaacctgg ctatttgctc actggaaaaa agacaattaa gtgcttatct 540
tcaggagact gggatggtgt catcccgaca tgcaaagagg cccagtgtga acatccagga 600
aagtttccca atgggcaggt aaaggaacct ctgagccttc aggttggcac aactgtgtac 660
ttctcctgta atgaagggta ccaattacaa ggacaaccct ctagtcagtg tgtaattgtt 720
gaacagaaag ccatctggac taagaagcca gtatgtaaag aaattctctg cccaccacct 780
ccacctgttc gtaatggaag tcatacaggc agcttttcag aaaatgtacc atatggaagc 840
acagttacct acacctgtga cccaagccca gagaaaggcg tgagcttcac tcttattgga 900
gagaagacta tcaattgtac tactggtagt cagaagactg ggatctggag tggccctgct 960
ccatattgtg tactttcaac ttctgcagtt ctgtgtttac aaccgaagat caaaagaggg 1020
caaatattat ctattttgaa agatagttat tcatataatg acactgtggc attttcttgt 1080
gaacctggct tcaccttgaa gggcaacagg agcattcgat gcaatgctca tggcacatgg 1140
gagccaccgg taccagtgtg tgaaaaagga tgtcaggctc ctcctaaaat tatcaatggg 1200
caaaagaag atagttactt gctcaacttt gaccctggta catccataag atatagctgt 1260
gaccctggct atttactggt gggagaggac actatacatt gcaccccctga ggggaagtgg 1320
acacccatta ctccccagtg cacagttgca gagtgtaagc cagtaggacc acatctcttt 1380
aagaggcctc agaatcagtt tattaggaca gctgttaatt cttcttgtga tgaagggttc 1440
cagttaagtg agagtgctta tcaactgtgt caaggtacaa ttccttggtt tatagaaatc 1500
cgtctttgta aagaaatcac ctgcccacca cctcctgtta tacacaacgg gacacataca 1560
tggagttcct cagaagatgt cccatatgga actgtggtca catacatgtg ctatcctggg 1620
ccagaggaag gcgtaaaatt caaactcatc ggggagcaaa ccatccactg tacaagtgac 1680
agcagaggaa gaggctcctg gagtagccct gctcctctct gtaaactttc cctcccagct 1740
gtccagtgca cagacgttca tgttgaaaat ggagtcaagc tcactgacaa taaagcccca 1800
tatttctaca atgatagtgt gatgttcaag tgtgatgatg gatatatttt gagtggaagc 1860
agtcagatcc ggtgtaaagc caataataac tgggatcctg aaaaaccact ttgtaaaaaa 1920
gaaggatgtg agcctatgag agtacatggc cttccagatg attcacatat aaaaactagtg 1980
aaaagaacct gtcaaaatgg gtaccagttg actggatata cttatgagaa gtgtcaaaat 2040
gctgagaatg ggacttggtt taaaaagatt gaagtttgta cagttattct ctgtcaacct 2100
ccaccaaaaa ttgcaaatgg tggtcacaca ggcatgatgg caaagcactt cctatatgga 2160
aatgaagttt cttatgaatg tgatgaaggg ttctatcttt tgggagagaa aagtttgcag 2220
tgcgtaaatg attctaaagg tcatggctct tggagtggac ctccaccaca atgcttacaa 2280
tcttctcctc taactcattg ccccgatcca gaagtcaaac atggttacaa actcaataaa 2340
actcattctg catttttctca taatgacata gtacattttg tctgcaatca aggcttcatc 2400
atgaacggca gccacttgat aaggtgtcat actaataaca catggttacc aggtgtacca 2460
acttgtatca gaaaggcttc tttagggtgt cagtctccat ccacaatccc caatgggaat 2520
catactggtg ggagtatagc tcgatttccc cctggaatgt cagtcatgta cagttgctac 2580
caaggcttcc ttatggctgg agaggcacgt cttatctgta ctcatgaggg tacctggagt 2640
caacctcccc cttttgcaa agaggtaaac tgtagcttcc ctgaagatac aaatggaatc 2700
cagaagggat ttcaacctgg gaaaacctat cgatttgggg ctactgtgac tctgaatgt 2760
gaggatgggt ataccttgga gggaagtccc cagagccagt gccaggatga cagccaatgg 2820
aaccctccct tggctctttg caaataccgt aggtggtcaa ctattcctct tatttgtggt 2880
atttctgtgg gctcagcact tatcattttg atgagtgtcg gcttctgtat gatattaaaa 2940
cacagagaaa gcaattatta tacaaagaca agacccaaag aaggagctct tcatttagaa 3000
acacgagaag tatattctat tgatccatat aacccagcaa gc              3042
```

```
<210> 28
<211> 1014
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 28
Ile Ser Cys Asp Pro Pro Pro Glu Val Lys Asn Ala Arg Lys Pro Tyr
1               5                   10                  15
Tyr Ser Leu Pro Ile Val Pro Gly Thr Val Leu Arg Tyr Thr Cys Ser
            20                  25                  30
```

```
Pro Ser Tyr Arg Leu Ile Gly Glu Lys Ala Ile Phe Cys Ile Ser Glu
        35              40                  45
Asn Gln Val His Ala Thr Trp Asp Lys Ala Pro Pro Ile Cys Glu Ser
    50              55                  60
Val Asn Lys Thr Ile Ser Cys Ser Asp Pro Ile Val Pro Gly Gly Phe
65                  70                  75                      80
Met Asn Lys Gly Ser Lys Ala Pro Phe Arg His Gly Asp Ser Val Thr
                85                  90                  95
Phe Thr Cys Lys Ala Asn Phe Thr Met Lys Gly Ser Lys Thr Val Trp
            100                 105                 110
Cys Gln Ala Asn Glu Met Trp Gly Pro Thr Ala Leu Pro Val Cys Glu
        115                 120                 125
Ser Asp Phe Pro Leu Glu Cys Pro Ser Leu Pro Thr Ile His Asn Gly
    130                 135                 140
His His Thr Gly Gln His Val Asp Gln Phe Val Ala Gly Leu Ser Val
145             150                 155                     160
Thr Tyr Ser Cys Glu Pro Gly Tyr Leu Leu Thr Gly Lys Lys Thr Ile
                165                 170                 175
Lys Cys Leu Ser Ser Gly Asp Trp Asp Gly Val Ile Pro Thr Cys Lys
            180                 185                 190
Glu Ala Gln Cys Glu His Pro Gly Lys Phe Pro Asn Gly Gln Val Lys
        195                 200                 205
Glu Pro Leu Ser Leu Gln Val Gly Thr Thr Val Tyr Phe Ser Cys Asn
    210                 215                 220
Glu Gly Tyr Gln Leu Gln Gly Gln Pro Ser Ser Gln Cys Val Ile Val
225             230                 235                     240
Glu Gln Lys Ala Ile Trp Thr Lys Lys Pro Val Cys Lys Glu Ile Leu
            245                 250                 255
Cys Pro Pro Pro Pro Val Arg Asn Gly Ser His Thr Gly Ser Phe
            260                 265                 270
Ser Glu Asn Val Pro Tyr Gly Ser Thr Val Thr Tyr Thr Cys Asp Pro
    275                 280                 285
Ser Pro Glu Lys Gly Val Ser Phe Thr Leu Ile Gly Glu Lys Thr Ile
    290                 295                 300
Asn Cys Thr Thr Gly Ser Gln Lys Thr Gly Ile Trp Ser Gly Pro Ala
305                 310                 315                     320
Pro Tyr Cys Val Leu Ser Thr Ser Ala Val Leu Cys Leu Gln Pro Lys
            325                 330                 335
Ile Lys Arg Gly Gln Ile Leu Ser Ile Leu Lys Asp Ser Tyr Ser Tyr
            340                 345                 350
Asn Asp Thr Val Ala Phe Ser Cys Glu Pro Gly Phe Thr Leu Lys Gly
        355                 360                 365
Asn Arg Ser Ile Arg Cys Asn Ala His Gly Thr Trp Glu Pro Pro Val
    370                 375                 380
Pro Val Cys Glu Lys Gly Cys Gln Ala Pro Pro Lys Ile Ile Asn Gly
385                 390                 395                     400
Gln Lys Glu Asp Ser Tyr Leu Leu Asn Phe Asp Pro Gly Thr Ser Ile
                405                 410                 415
Arg Tyr Ser Cys Asp Pro Gly Tyr Leu Leu Val Gly Glu Asp Thr Ile
            420                 425                 430
His Cys Thr Pro Glu Gly Lys Trp Thr Pro Ile Thr Pro Gln Cys Thr
        435                 440                 445
Val Ala Glu Cys Lys Pro Val Gly Pro His Leu Phe Lys Arg Pro Gln
    450                 455                 460
Asn Gln Phe Ile Arg Thr Ala Val Asn Ser Ser Cys Asp Glu Gly Phe
465                 470                 475                     480
Gln Leu Ser Glu Ser Ala Tyr Gln Leu Cys Gln Gly Thr Ile Pro Trp
                485                 490                 495
Phe Ile Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro Pro Pro Pro
            500                 505                 510
```

```
Val Ile His Asn Gly Thr His Thr Trp Ser Ser Ser Glu Asp Val Pro
        515                     520                 525
Tyr Gly Thr Val Val Thr Tyr Met Cys Tyr Pro Gly Pro Glu Glu Gly
        530                     535                 540
Val Lys Phe Lys Leu Ile Gly Glu Gln Thr Ile His Cys Thr Ser Asp
545                     550                 555                 560
Ser Arg Gly Arg Gly Ser Trp Ser Ser Pro Ala Pro Leu Cys Lys Leu
                565                 570                 575
Ser Leu Pro Ala Val Gln Cys Thr Asp Val His Val Glu Asn Gly Val
            580                 585                 590
Lys Leu Thr Asp Asn Lys Ala Pro Tyr Phe Tyr Asn Asp Ser Val Met
        595                 600                 605
Phe Lys Cys Asp Asp Gly Tyr Ile Leu Ser Gly Ser Ser Gln Ile Arg
        610                 615                 620
Cys Lys Ala Asn Asn Thr Trp Asp Pro Glu Lys Pro Leu Cys Lys Lys
625                 630                 635                 640
Glu Gly Cys Glu Pro Met Arg Val His Gly Leu Pro Asp Asp Ser His
                645                 650                 655
Ile Lys Leu Val Lys Arg Thr Cys Gln Asn Gly Tyr Gln Leu Thr Gly
            660                 665                 670
Tyr Thr Tyr Glu Lys Cys Gln Asn Ala Glu Asn Gly Thr Trp Phe Lys
        675                 680.                685
Lys Ile Glu Val Cys Thr Val Ile Leu Cys Gln Pro Pro Pro Lys Ile
        690                 695                 700
Ala Asn Gly Gly His Thr Gly Met Met Ala Lys His Phe Leu Tyr Gly
705                 710                 715                 720
Asn Glu Val Ser Tyr Glu Cys Asp Glu Gly Phe Tyr Leu Leu Gly Glu
                725                 730                 735
Lys Ser Leu Gln Cys Val Asn Asp Ser Lys Gly His Gly Ser Trp Ser
            740                 745                 750
Gly Pro Pro Pro Gln Cys Leu Gln Ser Ser Pro Leu Thr His Cys Pro
        755                 760                 765
Asp Pro Glu Val Lys His Gly Tyr Lys Leu Asn Lys Thr His Ser Ala
        770                 775                 780
Phe Ser His Asn Asp Ile Val His Phe Val Cys Asn Gln Gly Phe Ile
785                 790                 795                 800
Met Asn Gly Ser His Leu Ile Arg Cys His Thr Asn Asn Thr Trp Leu
                805                 810                 815
Pro Gly Val Pro Thr Cys Ile Arg Lys Ala Ser Leu Gly Cys Gln Ser
            820                 825                 830
Pro Ser Thr Ile Pro Asn Gly Asn His Thr Gly Gly Ser Ile Ala Arg
        835                 840                 845
Phe Pro Pro Gly Met Ser Val Met Tyr Ser Cys Tyr Gln Gly Phe Leu
        850                 855                 860
Met Ala Gly Glu Ala Arg Leu Ile Cys Thr His Glu Gly Thr Trp Ser
865                 870                 875                 880
Gln Pro Pro Pro Phe Cys Lys Glu Val Asn Cys Ser Phe Pro Glu Asp
                885                 890                 895
Thr Asn Gly Ile Gln Lys Gly Phe Gln Pro Gly Lys Thr Tyr Arg Phe
            900                 905                 910
Gly Ala Thr Val Thr Leu Glu Cys Glu Asp Gly Tyr Thr Leu Glu Gly
        915                 920                 925
Ser Pro Gln Ser Gln Cys Gln Asp Asp Ser Gln Trp Asn Pro Pro Leu
        930                 935                 940
Ala Leu Cys Lys Tyr Arg Arg Trp Ser Thr Ile Pro Leu Ile Cys Gly
945                 950                 955                 960
Ile Ser Val Gly Ser Ala Leu Ile Ile Leu Met Ser Val Gly Phe Cys
                965                 970                 975
Met Ile Leu Lys His Arg Glu Ser Asn Tyr Tyr Thr Lys Thr Arg Pro
            980                 985                 990
```

```
Lys Glu Gly Ala Leu His Leu Glu Thr Arg Glu Val Tyr Ser Ile Asp
        995                  1000                 1005
Pro Tyr Asn Pro Ala Ser
    1010
```

```
<210> 29
<211> 1033
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 29
Met Gly Ala Ala Gly Leu Leu Gly Val Phe Leu Ala Leu Val Ala Pro
 1               5                  10                 15
Gly Val Leu Gly Ile Ser Cys Gly Ser Pro Pro Pro Val Leu Asn Gly
        20                  25                 30
Arg Ile Ser Tyr Tyr Ser Thr Pro Ile Ala Val Gly Thr Val Ile Arg
        35                  40                 45
Tyr Ser Cys Ser Gly Thr Phe Arg Leu Ile Gly Glu Lys Ser Leu Leu
    50                  55                 60
Cys Ile Thr Lys Asp Lys Val Asp Gly Thr Trp Asp Lys Pro Ala Pro
65                  70                 75                 80
Lys Cys Glu Tyr Phe Asn Lys Tyr Ser Ser Cys Pro Glu Pro Ile Val
                85                  90                 95
Pro Gly Gly Tyr Lys Ile Arg Gly Ser Thr Pro Tyr Arg His Gly Asp
            100                 105                110
Ser Val Thr Phe Ala Cys Lys Thr Asn Phe Ser Met Asn Gly Asn Lys
            115                 120                125
Ser Val Trp Cys Gln Ala Asn Asn Met Trp Gly Pro Thr Arg Leu Pro
    130                 135                 140
Thr Cys Val Ser Val Phe Pro Leu Glu Cys Pro Ala Leu Pro Met Ile
145                 150                 155                160
His Asn Gly His His Thr Ser Glu Asn Val Gly Ser Ile Ala Pro Gly
                165                 170                175
Leu Ser Val Thr Tyr Ser Cys Glu Ser Gly Tyr Leu Leu Val Gly Glu
            180                 185                 190
Lys Ile Ile Asn Cys Leu Ser Ser Gly Lys Trp Ser Ala Val Pro Pro
        195                 200                 205
Thr Cys Glu Glu Ala Arg Cys Lys Ser Leu Gly Arg Phe Pro Asn Gly
    210                 215                 220
Lys Val Lys Glu Pro Pro Ile Leu Arg Val Gly Val Thr Ala Asn Phe
225                 230                 235                240
Phe Cys Asp Glu Gly Tyr Arg Leu Gln Gly Pro Pro Ser Ser Arg Cys
                245                 250                 255
Val Ile Ala Gly Gln Gly Val Ala Trp Thr Lys Met Pro Val Cys Glu
            260                 265                 270
Glu Ile Phe Cys Pro Ser Pro Pro Pro Ile Leu Asn Gly Arg His Ile
            275                 280                 285
Gly Asn Ser Leu Ala Asn Val Ser Tyr Gly Ser Ile Val Thr Tyr Thr
        290                 295                 300
Cys Asp Pro Asp Pro Glu Glu Gly Val Asn Phe Ile Leu Ile Gly Glu
305                 310                 315                320
Ser Thr Leu Arg Cys Thr Val Asp Ser Gln Lys Thr Gly Thr Trp Ser
                325                 330                 335
Gly Pro Ala Pro Arg Cys Glu Leu Ser Thr Ser Ala Val Gln Cys Pro
            340                 345                 350
```

```
His Pro Gln Ile Leu Arg Gly Arg Met Val Ser Gly Gln Lys Asp Arg
        355                     360                 365
Tyr Thr Tyr Asn Asp Thr Val Ile Phe Ala Cys Met Phe Gly Phe Thr
    370                     375                 380
Leu Lys Gly Ser Lys Gln Ile Arg Cys Asn Ala Gln Gly Thr Trp Glu
385                     390                 395                 400
Pro Ser Ala Pro Val Cys Glu Lys Glu Cys Gln Ala Pro Pro Asn Ile
                405                 410                 415
Leu Asn Gly Gln Lys Glu Asp Arg His Met Val Arg Phe Asp Pro Gly
        420                     425                 430
Thr Ser Ile Lys Tyr Ser Cys Asn Pro Gly Tyr Val Leu Val Gly Glu
        435                     440                 445
Glu Ser Ile Gln Cys Thr Ser Glu Gly Val Trp Thr Pro Pro Val Pro
    450                     455                 460
Gln Cys Lys Val Ala Ala Cys Glu Ala Thr Gly Arg Gln Leu Leu Thr
465                     470                 475                 480
Lys Pro Gln His Gln Phe Val Arg Pro Asp Val Asn Ser Ser Cys Gly
                485                 490                 495
Glu Gly Tyr Lys Leu Ser Gly Ser Val Tyr Gln Glu Cys Gln Gly Thr
        500                     505                 510
Ile Pro Trp Phe Met Glu Ile Arg Leu Cys Lys Glu Ile Thr Cys Pro
        515                     520                 525
Pro Pro Pro Val Ile Tyr Asn Gly Ala His Thr Gly Ser Ser Leu Glu
    530                     535                 540
Asp Phe Pro Tyr Gly Thr Thr Val Thr Tyr Thr Cys Asn Pro Gly Pro
545                     550                     555                 560
Glu Arg Gly Val Glu Phe Ser Leu Ile Gly Glu Ser Thr Ile Arg Cys
                565                     570                 575
Thr Ser Asn Asp Gln Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu
        580                     585                 590
Cys Lys Leu Ser Leu Leu Ala Val Gln Cys Ser His Val His Ile Ala
        595                     600                 605
Asn Gly Tyr Lys Ile Ser Gly Lys Glu Ala Pro Tyr Phe Tyr Asn Asp
    610                     615                 620
Thr Val Thr Phe Lys Cys Tyr Ser Gly Phe Thr Leu Lys Gly Ser Ser
625                     630                 635                 640
Gln Ile Arg Cys Lys Ala Asp Asn Thr Trp Asp Pro Glu Ile Pro Val
                645                 650                 655
Cys Glu Lys Glu Thr Cys Gln His Val Arg Gln Ser Leu Gln Glu Leu
                660                 665                 670
Pro Ala Gly Ser Arg Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly
        675                     680                 685
Tyr Gln Leu Thr Gly His Ala Tyr Gln Met Cys Gln Asp Ala Glu Asn
    690                     695                 700
Gly Ile Trp Phe Lys Lys Ile Pro Leu Cys Lys Val Ile His Cys His
705                     710                 715                 720
Pro Pro Pro Val Ile Val Asn Gly Lys His Thr Gly Met Met Ala Glu
                725                 730                 735
Asn Phe Leu Tyr Gly Asn Glu Val Ser Tyr Glu Cys Asp Gln Gly Phe
            740                 745                 750
Tyr Leu Leu Gly Glu Lys Lys Leu Gln Cys Arg Ser Asp Ser Lys Gly
        755                     760                 765
His Gly Ser Trp Ser Gly Pro Ser Pro Gln Cys Leu Arg Ser Pro Pro
    770                     775                 780
Val Thr Arg Cys Pro Asn Pro Glu Val Lys His Gly Tyr Lys Leu Asn
785                     790                 795                 800
Lys Thr His Ser Ala Tyr Ser His Asn Asp Ile Val Tyr Val Asp Cys
                805                 810                 815
Asn Pro Gly Phe Ile Met Asn Gly Ser Arg Val Ile Arg Cys His Thr
        820                     825                 830
```

```
Asp Asn Thr Trp Val Pro Gly Val Pro Thr Cys Met Lys Lys Ala Phe
        835             840             845
Ile Gly Cys Pro Pro Pro Pro Lys Thr Pro Asn Gly Asn His Thr Gly
    850             855             860
Gly Asn Ile Ala Arg Phe Ser Pro Gly Met Ser Ile Leu Tyr Ser Cys
865             870             875             880
Asp Gln Gly Tyr Leu Leu Val Gly Glu Ala Leu Leu Leu Cys Thr His
            885             890             895
Glu Gly Thr Trp Ser Gln Pro Ala Pro His Cys Lys Glu Val Asn Cys
        900             905             910
Ser Ser Pro Ala Asp Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg
    915             920             925
Lys Met Tyr Gln Tyr Gly Ala Val Val Thr Leu Glu Cys Glu Asp Gly
    930             935             940
Tyr Met Leu Glu Gly Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln
945             950             955             960
Trp Asn Pro Pro Leu Ala Val Cys Arg Ser Arg Ser Leu Ala Pro Val
            965             970             975
Leu Cys Gly Ile Ala Ala Gly Leu Ile Leu Leu Thr Phe Leu Ile Val
            980             985             990
Ile Thr Leu Tyr Val Ile Ser Lys His Arg Glu Arg Asn Tyr Tyr Thr
    995             1000            1005
Asp Thr Ser Gln Lys Glu Ala Phe His Leu Glu Ala Arg Glu Val Tyr
    1010            1015            1020
Ser Val Asp Pro Tyr Asn Pro Ala Ser
1025            1030
```